An Integrative Personalized Approach to Diagnostics and Drug Discovery
What We Do

Our world-class algorithms enable us to analyze genetic mutations and produce the most precise diagnostics available for the patient. We also collaborate with Pharma to accelerate drug repurposing & discovery for a variety of diseases.
The Process

**Step 1: Sample Preparation**
We obtain the DNA of the patient through a painless saliva sample.

**Step 2: Sequencing**
Our partner, BGI, sequences the exome of the patient to identify genes that might be responsible for disease and these proteins serve as our drug targets.

**Step 3: Physicians and Pharma**
We recommend treatment options to the patient’s physician and/or partner with Pharma on the novel compound, reducing time to patient utilization.
A Two-Sided Approach to Personalized Medicine

**Diagnostics**
- Exome sequencing and interpretation, including prediction of disease-associated mutations, drug selection & avoidance, and drug metabolism

**Precision Medicine**
- Utilizing our algorithms to identify existing and new compounds that can treat disease-causing mutations.
- Partner with Pharma to accelerate drug repurposing & discovery
Our Algorithms

Prognostix is the first algorithm capable of covering whole exomes, and uses 3D protein structure to make more precise predictions about a DNA mutation’s possible pathogenicity.

Dr. Prodis makes predictions of protein structure, ligand binding sites, prediction of FDA binding drugs, side effects and toxicity for 86% of the human proteome.

Findsite utilizes ligand homology screening; it is industry leading and capable of predicting structures of a large portion of the human proteome, allowing high-throughput drug screening.
Comparison of Prognostix to Other Algorithms

Accuracy

Prognostix significantly outperforms competing algorithms:

**MCC**
- the ability of the algorithm to correctly sort pathogenic mutations from non-pathogenic

**AUC**
- the ratio of true positives to false positives

**Accuracy**
- the ability to correctly identify pathogenic mutations

When run on a 1K genome with 150,000 mutations, the false positive rate was <10%, which is significantly lower than other methods

See Appendix A
Comparison of Findsite to Other Algorithms

**Accuracy**
- When screening proteins against true matching ligands, decoy ligands, and unrelated ligands, Findsite will correctly identify more true matching ligands for a protein in the top 1% of identified ligands as compared to competitive methods.
- The ratio of true positives to false positives is significantly higher than competing methods.

**Speed**
- When screened across a 325 bp protein, FINDSITEcomb was able to screen 1000 compounds in 30 hours.
- **25.6 compounds/hour** faster than DOCK 6
- **33x** faster than AUTODOCKvina
- **167x** faster than DOCK 6

See Appendix B
Partnership with BGI

Enhanced Accelerated Exome – Launched November 2014

- Combine BGI's infrastructure with expertise of Intellimedix to offer both NGS analysis and genome-wide diagnostic interpretation faster than current industry norms
- Provide extremely fast turnaround with a high quality product
  - More comprehensive analysis than currently available in the market
  - Researchers - and soon clinicians - will be able to leverage service to gain detailed understanding of patient-specific genetic conditions
- Redefine customer service in exome marketplace, setting a new standard across the genomic sequencing and interpretation industry
- Save time and increase the specificity of analysis, giving patients better diagnostics, and eventually, more successful therapeutics
Our Competitive Advantage

**Diagnostics**

- Speed to results: 10 day turnaround (vs 8 weeks)
- Accuracy: 3x lower rate of false positives
- Greater coverage: 80% exome coverage (vs 30%)

**Precision Medicine**

- Accuracy and coverage: higher than existing standards
- Time compression: algorithms, FDA-approved drugs
Intellimedix Current Applications

High-Throughput Screening Approach Currently Being Used for Epilepsy (Dravet) and Mitochondrial Disorders

- Genome and Exome Sequencing
- Prognostix tool for identification of known and possible disease-causing mutations
- \textit{In silico} screening of FDA and non-FDA approved compounds
- Predictions of potential efficacy, side effects and toxicity
- High-throughput screening of drugs in personalized \textit{in vitro} models (IPSCS) and single cell models to confirm activity on predicted molecular targets
- Phase I or Phase II clinical trials of most promising drugs
Our Proof of Concept

Proof of Concept and Intellectual Property

• 2 repurposed drugs for Chronic Fatigue Syndrome
• 4 repurposed drugs for Dravet Syndrome
• Provisional patents for 52 anti-Ebola molecules
• Other patents pending

Unique Assets & Capabilities

• Exclusive software license of our algorithms

Partners & Collaborators

• BGI – gene sequencing; cancer panel and drug repurposing; Alzheimer’s diagnostic
• Pfizer/EF – precision drug discovery for epilepsy
• CDC/Emory University – anti-Ebola compounds
Accelerating Timeline

- Series A Financing
- Pfizer/EF Project
- Virus Collaboration
- Exome Product
- BGI Partnership
- GA Tech License
- Kytril Discovery
- 4 Novel AED Compounds Discovered
- Dravet Research

2012 | 2013 | 2014 | 2015
---|---|---|---
Algorithms
The Team

Jim Richards
President & CEO

Jeffery Skolnick, PhD
Director Systems Biology at Georgia Tech; 325 publications; Google Scholar h-index: 73

Harvey Kupferberg, PharmD, PhD
Leader of NIH’s Antiepileptic Drug Development program
The Business Model

Diagnostics:

- Diagnostic report for patients (disease prediction, drug selection & avoidance, drug metabolism, etc)

Precision Medicine:

- Scientific services to pharma (Pfizer/Epilepsy Foundation)
- Royalty on drugs repurposed or developed
# Intellimedix Projected Income Statement

<table>
<thead>
<tr>
<th>$ Amounts in Millions</th>
<th>Year</th>
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<tbody>
<tr>
<td></td>
<td>2015</td>
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<tr>
<td><strong>Revenue:</strong></td>
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<tr>
<td>Diagnostics Revenue</td>
<td>$0.3</td>
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<tr>
<td>Precision Medicine Revenues</td>
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<tr>
<td><strong>Total Revenues</strong></td>
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<tr>
<td><strong>Total Cost of Goods Sold</strong></td>
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<td><strong>Gross Margin</strong></td>
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<td><strong>Total Operating Expenses</strong></td>
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<td><strong>EBITDA</strong></td>
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<tr>
<td><strong>Cash Flow</strong></td>
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## Appendix A

### PredictSNP Benchmark Set

<table>
<thead>
<tr>
<th>Method</th>
<th># of Mutations</th>
<th>False Positive Rate</th>
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<tr>
<td>PROGNOSTIX</td>
<td>156,273</td>
<td>6.68%</td>
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<tr>
<td>SIFT</td>
<td>147,808</td>
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<tr>
<td>PPH2_HDIV</td>
<td>147,792</td>
<td>48.9%</td>
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<td>MUTATIONASSESSOR*</td>
<td>145,062</td>
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<tr>
<td>FATHMM*</td>
<td>130,043</td>
<td>13.6%</td>
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Appendix B

# True Binding Compounds Found in Top 1%

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<tr>
<td>AUTODO...</td>
<td>0</td>
</tr>
<tr>
<td>DOCK 6</td>
<td>0</td>
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ratio of True Positives to False Positives

<table>
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<tr>
<th>Method</th>
<th>AUAC</th>
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<tr>
<td>FINDSITEcomb</td>
<td>0.77</td>
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<tr>
<td>SURFLEX</td>
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<tr>
<td>PhDOCK</td>
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<td>ICM</td>
<td>0.61</td>
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<tr>
<td>FLEXX</td>
<td>0.60</td>
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<tr>
<td>DOCK 6</td>
<td>0.59</td>
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